CLAIMS

1. Method for acquiring binding structure(s) against a target structure by means of a first library of binding structure(s) linked to genetic and/or other identifying information, c h a r a c t e r i z e d by the steps of
(a) reacting the first library with the displayed target structure to bind some of the binding structures to the displayed target structure;
(b) separating the displayed target structure and bound binding structures from unbound binding structures;
(c) recovering bound or unbound binding structures; and
(d) amplifying bound or unbound binding structures to create a second enriched library of binding structures;
the displayed target structure being displayed *in vivo* and/or *in situ*.

2. Method as claimed in claim 1, c h a r a c t e r i z e d in that the steps (a) through (c) are repeated.

3. Method as claimed in claim 1, c h a r a c t e r i z e d in that the steps (a) through (d) are repeated.

4. Method as claimed in ~~any of claims 1-3~~, c h a r a c t e r i z e d in that monoclonal, single-entity, honogenous, uniform and/or other binding structures are isolated and/or amplified from the second, or third, or fourth etc enriched library.

5. Method as claimed in ~~any of claims 1-4~~, c h a r a c t e r i z e d in that the binding structure(s) comprise(s) monoclonal antibody(ies), protein(s), peptide(s), or organochemical entity(ies).

6. Method as claimed in ~~any preceding claim~~, characterized in that the displayed target structure includes previously uncharacterized and/or unpurified and/or unknown molecules.

7. Method as claimed in ~~any preceding claim~~, characterized in that the displayed target structure is expressed as an authentic phenotypic epitope.

8. Method as claimed in ~~any preceding claim~~, characterized in that the displayed target structure is obtained within a set of target structures representing ~~the authentic~~ *in-vivo* and/or *in situ* phenotype.

9. Method as claimed in claim 8, characterized in that the authentic *in vivo* and/or *in situ* phenotype is the result of a physiological process, a pathological process, a cell and/or tissue development and differentiation, or a drug response, or a naturally occurring degradation process.

10. Method as claimed in claim 9, characterized in that the pathological process is an inflammation, a secondary tumor deposit, or tumor vasculature.

11. Method as claimed in claim 1, characterized in that the displayed target structure is obtained within a set of desired displayed target structures.

12. Method as claimed in claim 1 ~~or 11~~, characterized in that bound structures are recovered.

13. Method as claimed in claim 1 ~~or 11~~, characterized in that unbound structures are recovered.

14. Method as claimed in claim 1, characterized in that the displayed target structure is obtained within a set of undesired displayed target structures.

15. Method as claimed in claim 1 ~~or 14~~, characterized in that bound structures are recovered.

16. Method as claimed in claim 1 ~~or 14~~, characterized in that unbound structures are recovered.

17. Method as claimed in claim 7 ~~or 8~~, characterized in that the set of displayed target structures are target structures from a whole cell.

18. Method as claimed in claim 7 ~~or 8~~, characterized in that the displayed target structure is located in a cell surface.

19. Method as claimed in claim 7 ~~or 8~~, characterized in that the displayed target structure is located intracellularly of a cell surface.

20. Method as claimed in claim 7 ~~or 8~~, characterized in that the displayed target structure is located extracellularly of a cell surface.

21. Method as claimed in claim 7 ~~or 8~~, characterized in that the displayed target structure is located intranuclear of a nuclear membrane.

22. Method as claimed in claim 7 ~~or 8~~, characterized in that the displayed target structure comprises the whole and/or a portion and/or a set of (an) antigen(s), (an) epitope(s), (a) ligand(s), (a) receptor(s), (an) adhesion molecule(s), (a) matrix molecule(s) and/or (a) matrix associated molecule(s).

23. Method as claimed in claim 1, characterized in that the displayed target structure is based on protein, carbohydrate, nucleic acid, or lipid.

24. Method as claimed in claim 8 ~~or 9~~, characterized in that the authentic *in vivo* and/or *in situ* phenotype authentic is obtained from tissue sections by a histological technique.

25. Method as claimed in claim 24, characterized in that the histological technique comprises freezing and/or fixation, and sectioning of a tissue sample.

26. Method as claimed in claim 24, characterized in that the tissue sections are pre-treated with enzyme or by chemical means.

27. Method as claimed in claim 26, characterized in that the enzyme pre-treatment is performed with a protease and/or a polysaccharase and/or ribonuclease, and/or nuclease.

28. Method as claimed in claim 8 ~~or 9~~, characterized in that the authentic *in vivo* and/or *in situ* phenotype is obtained from body fluids.

29. Method as claimed in claim 28, characterized in that the body fluids comprise blood, suspension of bone marrow, lymph, sperm, cerebrospinal fluid, or secretions from cells.

30. Method as claimed in claim 29, characterized in that the secretions are secreted actively.

31. Method as claimed in claim 30, characterized in that the secretions contain cytokines.

32. Method as claimed in claim 29, characterized in that the secretions are secreted passively.

33. Method as claimed in claim 28, characterized in that the authentic *in vivo* and/or *in situ* phenotype is represented by suspended cells from a tissue, or a body fluid, or such cells pelleted.

34. Method as claimed in claim 8 ~~or 9~~, characterized in that the displayed target structure is a molecule released from cells.

35. Method as claimed in claim 34, characterized in that cells are tumor cells.

36. Method as claimed in claim 34 ~~or 35~~, characterized in that the molecule is released actively.

37. Method as claimed in claim 34 ~~or 35~~, characterized in that the molecule is released passively.

38. Method as claimed in claim 1, characterized in that the first library is a naive, synthetic or semi-synthetic antibody library.

39. Method as claimed in claim 1, characterized in that the first library is a combinatorial and/or preselected library.

40. Method as claimed in claim 39, characterized in that the combinatorial and/or preselected library is a library produced by immunization against one or more displayed target structures.

41. Method as claimed in claim 39, characterized in that the combinatorial and/or preselected library is a chemical library.

42. Method as claimed in claim 1, characterized in that the acquirement of binding structures comprises identifying, producing, characterizing, selecting, enriching, or defining such structures.

43. Method as claimed in ~~any preceding claim~~ claim 1, characterized in that the amplification of bound binding structures comprises synthesis in growing bacterial cells, PCR synthesis, and chemical synthesis.

44. Method as claimed in claim 1, characterized in that the linkage between binding structure(s) and genetic and/or other identifying information comprises coded beads or polysomes.

45. Method as claimed in claim 1, characterized in that the linkage between binding structure(s) and genetic and/or other identifying information comprises particles of a filamentous phage or of any other virus.

46. Method as claimed in claim 45, characterized in that the filamentous phage is bacteriophage M13.

47. Method as claimed in claim 1, characterized in that the recovering of bound binding structures comprises a cleavage.

48. Method as claimed in claim 47, characterized in that the cleavage site maintains the amplification ability.

49. Method as claimed in ~~any of claims 45-48~~ claim 45, characterized in that the cleavage site is between the binding structure and a phage protein.

50. Method as claimed in claim 49, characterized in that the phage protein is the minor coat protein pIII.

51. Method as claimed in claim 47, characterized in that the cleavage site is a recognition site for a protease.

52. Method as claimed in ~~any of claims 47-51,~~ claim 47 characterized in that the cleavage site is Ala-Ala-His-Tyr and the protease is Ala64-subtilisin. [SEQ ID NO:1]

53. Method as claimed in ~~any of claims 47-51,~~ claim 47 characterized in that the cleavage site is Ile-Glu-Gly-Arg and the protease is blood clotting factor Xa. [SEQ ID NO:2]

54. Method as claimed in claim 1, characterized in that the recovery of bound binding structures is effected by means of a chemically based elution.

55. Method as claimed in claim 54, characterized in that the elution is performed with an acid or alkaline solution, such as triethylamine.

56. Method as claimed in claim 6, characterized in that the antibody is the scFv C215 antibody fragment.

57. Method as claimed in claim 7, characterized in that the displayed target structure is the epitope on GA733-2 epithelial glycoprotein expressed in colorectal carcinoma.

58. Binding structures produced as claimed in ~~any of claims 1-57.~~ claim 1

59. The second, or third, or fourth etc enriched library of binding structures obtained by the method as claimed in ~~any of claims 1-3.~~ claim 1

60. Binding structures produced from the library as claimed in claim 59.